while the tags are not hybridized to the sequence regions that flank the target sequences. No new matter has been added by any of the amendments.

II. Rejections under 35 U.S.C. §102(b)

Claims 1, 2, 3, 5 and 8-12 were rejected as allegedly being anticipated by Grossman et al. (U.S. Patent No. 5,514,543). The rejection is respectfully traversed.

A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference. *Verdegaal Brothers Inc. v. Union Oil Co. of California,* 2 USPQ2d 1051, Fed. Cir. 1987. Inherency may not be established by probabilities or possibilities. The mere fact that a certain thing *may* result from a given set of circumstances is not sufficient. *Ex parte Skinner*, 2 USPQ2d 1788, BPAI 1987; *In re Oelrich and Divigard*, 666 F.2d 578, 212 USPQ 323, CCPA 1981.

Present claim 1 recites first and second complexes that are present in a mixture. Taking the first complex by way of example, the first complex comprises (1) a first probe comprising a first target-specific portion and a first tag, and (2) a first mobility-modifier comprising a first tail and a first tag complement for binding to the tag of the first probe. The first probe is designed to hybridize sequence specifically to a first target nucleic acid sequence. The tag is designed not to hybridize to the adjacent sequence regions that flank the first target sequence, when the first target-specific portion is sequence specifically hybridized to the first target nucleic acid sequence. Similar features apply to the second complex.

The Examiner asserted that claim 1 is anticipated by Grossman et al. at Figures 1A and 4A. In particular, the Examiner has equated probe 20 in Fig. 1A with the mobility modifiers recited in pending claim 1, and has equated target polynucleotide 26 with the recited probes. However, Figure 1A merely shows a tailed probe that is hybridized directly to a target polynucleotide, such as genomic DNA in single stranded form (e.g., see Grossman at column 7 lines 29-30), and Figure 4A merely illustrates attachment of a PEG tail to an oligonucleotide.

Even if, for the sake of argument, probe 20 is taken to have the features of the mobility modifiers recited in pending claim 1, polynucleotide 26 cannot be taken to be the same as the probes recited in claim 1 for at least the reason that there is no indication or suggestion in Fig. 1A, express or otherwise, that polynucleotide 26 should be designed so that region 24 (which the Examiner deems to be a "tag") does not hybridize to the regions that flank the target sequence

when the target-specific portion of the probe is specifically hybridized to its target nucleic acid sequence. Since the reference fails to teach each and every essential element of claim 1, there is no anticipation.

Nor would the claims have been obvious. Obviousness can only be established by modifying or combining the teachings of the prior art to produce the claimed invention where there is some teaching, suggestion, or motivation to do so found in either (1) the references themselves, or (2) in the knowledge generally available to one of ordinary skill in the art. *In re Fine*, 5 USPQ2d 1596, 1598, Fed. Cir. 1988. The mere fact that the prior art may be modified in a manner suggested by the Examiner does not make the modification obvious unless the prior art suggested the desirability of the modification. *In re Gordon et al.*, 221 USPQ 1126, Fed. Cir. 1984.

In the present case, there is no teaching, suggestion, or motivation to modify the teachings of Grossman et al. to arrive at the present invention. In particular, there is no suggestion of altering the complex shown in Figure 1A of Grossman et al. to produce a composition comprising first and second complexes in accordance with claim 1. Accordingly, Grossman et al. does render the present claims obvious.

III. Rejection under 35 U.S.C. §103

Claim 7 was rejected as allegedly being obvious over Grossman et al. (supra) in view of Buchardt et al. (Trends in Biotechnology 11:384-386 (1993).

The pertinence of Grossman et al. is discussed above. Nor are its deficiencies remedied by Buchardt et al., which was presumably cited for its general review of peptide nucleic acids (PNAs), but says nothing about compositions containing complexes of the type embodied in present claim 1.

Since parent claim 1 is patentable, so too are its dependent claims. Accordingly, withdrawal of the rejection is respectfully requested.

IV. Obviousness-Type Double-Patenting Rejection

The claims were provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 26, 4-10, 13 and 15-18 of Serr. No. 09/232,000 (now claims 1, 2-8, 11 and 13-16, respectively, in US Patent 6,432,642) in

view of Grossman et al. (supra). The Examiner indicated that the rejection would be obviated by a terminal disclaimer. Accordingly, a Terminal Disclaimer is enclosed herewith solely to obviate the rejection, but it is not to be construed as an admission or concession that the grounds of the rejection are valid. *Quad Environmental Technologies v Union Sanitary District* 20 USPQ2d 1392, Fed. Cir. 1991.

V. CONCLUSION

The applicant submits that the claims now pending in the present application are in condition for allowance. A Notice of Allowance is therefore respectfully requested.

VI. CONDITIONAL PETITION FOR TIME EXTENSION and FEE AUTHORIZATION

If any additional time extensions are required, such time extensions are hereby requested. If any additional fees not submitted with this response are required, please take such fees from deposit account number **01-2213**.

Respectfully submitted,

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Appendix Showing Markup of Changes
(Added text is indicated by bold and underlining)

1. (Twice Amended) A composition for detecting two or more target nucleic acid sequences comprising:

a first complex comprising:

a first probe comprising a first target-specific portion for sequence-specific hybridization to a first target nucleic acid sequence **that is flanked at each end by two adjacent sequence regions,** and a first tag **that is designed not to hybridize to said adjacent sequence regions when the first target-specific portion is sequence specifically hybridized to the first target nucleic acid sequence**; **and**

a first mobility-modifier comprising a first tail and a first tag complement for binding to the first tag; and

a second complex comprising:

a second probe comprising a second target-specific portion for sequence-specific hybridization to a second target nucleic acid sequence **that is flanked at each end by two adjacent sequence regions,** and a second tag **that is designed not to hybridize to the second said adjacent sequence regions when the second target-specific portion is sequence specifically hybridized to the second target nucleic acid sequence**; and

a second mobility-modifier comprising a second tail and a second tag complement for binding to the second tag;

wherein a mobility of the first complex in a mobility-dependent analysis technique is distinguishable from a mobility of the second complex in the mobility-dependent analysis technique; and

wherein the first complex and the second complex are present as a mixture.